<210>   1
<211>   1570
<212>   DNA
<213>   Trichoderma reesei

<400>   1
atgtatcgga agttggccgt catctcggcc ttcttggcca cagctcgtgc tcagtcggcc      60
tgcactctcc aatcggagac tcacccgcct ctgacatggc agaaatgctc gtctggtggc     120
acttgcactc aacagacagg ctccgtggtc atcgacgcca actggcgctg gactcacgct     180
acgaacagca gcacgaactg ctacgatggc aacacttgga gctcgaccct atgtcctgac     240
aacgagacct gcgcgaagaa ctgctgtctg gacggtgccg cctacgcgtc cacgtacgga     300
gttaccacga gcggtaacag cctctccatt ggctttgtca cccagtctgc gcagaagaac     360
gttggcgctc gcctttacct tatggcgagc gacacgacct accaggaatt caccctgctt     420
ggcaacgagt tctcttttcga tgttgatgtt tcgcagctgc cgtaagtgac ttaccatgaa     480
cccctgacgt atcttcttgt gggctcccag ctgactggcc aatttaaggt gcggcttgaa     540
cggagctctc tacttcgtgt ccatggacgc ggatggtggc gtgagcaagt atcccaccaa     600
caccgctggc gccaagtacg gcacggggta ctgtgacagc cagtgtcccc gcgatctgaa     660
gttcatcaat ggccaggcca acgttgaggg ctgggagccg tcatccaaca acgcaaacac     720
gggcattgga ggacacggaa gctgctgctc tgagatggat atctgggagg ccaactccat     780
ctccgaggct cttaccccc acccttgcac gactgtcggc caggagatct gcgagggtga     840
tgggtgcggc ggaacttact ccgataacag atatggcggc acttgcgatc ccgatggctg     900
cgactggaac ccataccgcc tgggcaacac cagcttctac ggccctggct caagctttac     960
cctcgatacc accaagaaat tgaccgttgt cacccagttc gagacgtcgg gtgccatcaa    1020
ccgatactat gtccagaatg gcgtcacttt ccagcagccc aacgccgagc ttggtagtta    1080
ctctggcaac gagctcaacg atgattactg cacagctgag gaggcagaat cggcggatc     1140
ctctttctca gacaagggcg gcctgactca gttcaagaag ctacctctg gcggcatggt    1200
tctggtcatg agtctgtggg atgatgtgag tttgatggac aaacatgcgc gttgacaaag    1260
agtcaagcag ctgactgaga tgttacagta ctacgccaac atgctgtggc tggactccac    1320
ctacccgaca aacgagacct cctccacacc cggtgccgtg cgcggaagct gctccaccag    1380
ctccggtgtc cctgctcagg tcgaatctca gtctcccaac gccaaggtca ccttctccaa    1440
catcaagttc ggacccattg gcagcaccgg caaccctagc ggcggcaacc ctcccggcgg    1500
aaacccgcct ggcaccacca ccacccgccg cccagccact accactggaa gctctcccgg    1560
acctactagt                                                          1570

<210>   2

<211> 51
<212> DNA
<213> Trichoderma reesei

<400> 2
atgtatcgga agttggccgt catctcggcc ttcttggcca cagctcgtgc t                51

<210> 3
<211> 1438
<212> DNA
<213> Trichoderma reesei

<400> 3
cagtcggcct gcactctcca atcggagact cacccgcctc tgacatggca gaaatgctcg      60
tctggtggca cttgcactca acagacaggc tccgtggtca tcgacgccaa ctggcgctgg      120
actcacgcta cgaacagcag cacgaactgc tacgatggca acacttggag ctcgacccta      180
tgtcctgaca acgagacctg cgcgaagaac tgctgtctgg acggtgccgc ctacgcgtcc      240
acgtacggag ttaccacgag cggtaacagc ctctccattg gctttgtcac ccagtctgcg      300
cagaagaacg ttggcgctcg cctttacctt atggcgagcg acacgaccta ccaggaattc      360
accctgcttg caacgagtt ctctttcgat gttgatgttt cgcagctgcc gtaagtgact      420
taccatgaac ccctgacgta tcttcttgtg ggctcccagc tgactggcca atttaaggtg      480
cggcttgaac ggagctctct acttcgtgtc catggacgcg gatggtggcg tgagcaagta      540
tcccaccaac accgctggcg ccaagtacgg cacggggtac tgtgacagcc agtgtccccg      600
cgatctgaag ttcatcaatg ccaggccaa cgttgagggc tgggagccgt catccaacaa      660
cgcaaacacg ggcattggag acacggaag ctgctgctct gagatggata tctgggaggc      720
caactccatc tccgaggctc ttacccccca cccttgcacg actgtcggcc aggagatctg      780
cgagggtgat gggtgcggcg gaacttactc cgataacaga tatggcggca cttgcgatcc      840
cgatggctgc gactggaacc cataccgcct gggcaacacc agcttctacg ccctggctc       900
aagctttacc ctcgatacca ccaagaaatt gaccgttgtc acccagttcg agacgtcggg      960
tgccatcaac cgatactatg tccagaatgg cgtcactttc cagcagccca cgccgagct      1020
tggtagttac tctggcaacg agctcaacga tgattactgc acagctgagg aggcagaatt      1080
cggcggatcc tctttctcag acaagggcgg cctgactcag ttcaagaagg ctacctctgg      1140
cggcatggtt ctggtcatga gtctgtggga tgatgtgagt ttgatggaca aacatgcgcg      1200
ttgacaaaga gtcaagcagc tgactgagat gttacagtac tacgccaaca tgctgtggct      1260
ggactccacc tacccgacaa acgagacctc ctccacaccc ggtgccgtgc gcggaagctg      ˙1320
ctccaccagc tccggtgtcc ctgctcaggt cgaatctcag tctcccaacg ccaaggtcac      1380
cttctccaac atcaagttcg acccattgg cagcaccggc aaccctagcg gcggcaac       1438

<210> 4
<211> 81
<212> DNA
<213> Trichoderma reesei

<400> 4
cctccccggcg gaaacccgcc tggcaccacc accacccgcc gcccagccac taccactgga      60
agctctcccg gacctactag t                                                81

<210> 5
<211> 480
<212> PRT
<213> Trichoderma reesei

<400> 5
Met Tyr Arg Lys Leu Ala Val Ile Ser Ala Phe Leu Ala Thr Ala Arg
1               5                   10                  15
Ala Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr

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              20                    25                    30
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
        35                    40                    45
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
        50                    55                    60
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
65                    70                    75                    80
Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
                85                    90                    95
Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
                100                   105                   110
Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
                115                   120                   125
Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
        130                   135                   140
Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
145                   150                   155                   160
Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
                165                   170                   175
Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
                180                   185                   190
Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
        195                   200                   205
Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
        210                   215                   220
Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
225                   230                   235                   240
Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
                245                   250                   255
Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
                260                   265                   270
Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
        275                   280                   285
Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
        290                   295                   300
Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
305                   310                   315                   320
Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
                325                   330                   335
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
                340                   345                   350
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
                355                   360                   365
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
        370                   375                   380
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
385                   390                   395                   400
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
                405                   410                   415
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
                420                   425                   430
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
                435                   440                   445
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
        450                   455                   460
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Ser
465                   470                   475                   480
```

<210> 6
<211> 431
<212> PRT
<213> Trichoderma reesei

<400> 6
Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1               5                   10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
                20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
            35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
        50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
                100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
            115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
            195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
            275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                325                 330                 335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
                340                 345                 350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
                355                 360                 365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
    370                 375                 380
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                 390                 395                 400

```
Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
                405                 410                 415
Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
                420                 425                 430


<210>   7
<211>   1077
<212>   DNA
<213>   Acidothermus cellulolyticus

<400>   7
gcgggcggcg gctattggca cacgagcggc cgggagatcc tggacgcgaa caacgtgccg       60
gtacggatcg ccggcatcaa ctggtttggg ttcgaaacct gcaattacgt cgtgcacggt      120
ctctggtcac gcgactaccg cagcatgctc gaccagataa agtcgctcgg ctacaacaca      180
atccggctgc cgtactctga cgacattctc aagccgggca ccatgccgaa cagcatcaat      240
ttttaccaga tgaatcagga cctgcagggt ctgacgtcct tgcaggtcat ggacaaaatc      300
gtcgcgtacg ccggtcagat cggcctgcgc atcattcttg accgccaccg accggattgc      360
agcgggcagt cggcgctgtg gtacacgagc agcgtctcgg aggctacgtg gatttccgac      420
ctgcaagcgc tggcgcagcg ctacaaggga aacccgacgg tcgtcggctt tgacttgcac      480
aacgagccgc atgacccggc ctgctggggc tgcggcgatc cgagcatcga ctggcgattg      540
gccgccgagc gggccggaaa cgccgtgctc tcggtgaatc cgaacctgct cattttcgtc      600
gaaggtgtgc agagctacaa cggagactcc tactggtggg cgggcaacct gcaaggagcc      660
ggccagtacc cggtcgtgct gaacgtgccg aaccgcctgg tgtactcggc cacgactac      720
gcgacgagcg tctacccgca cgtggttc agcgatccga ccttccccaa caacatgccc      780
ggcatctgga caagaactg gggatacctc ttcaatcaga acattgcacc ggtatggctg      840
ggcgaattcg gtacgacact gcaatccacg accgaccaga cgtggctgaa gacgctcgtc      900
cagtacctac ggccgaccgc gcaatacggt gcggacagct ccagtggac cttctggtcc      960
tggaaccccg attccggcga cacaggagga attctcaagg atgactggca gacggtcgac     1020
acagtaaaag acggctatct cgcgccgatc aagtcgtcga ttttcgatcc tgtcggc       1077


<210>   8
<211>   359
<212>   PRT
<213>   Acidothermus cellulolyticus

<400>   8
Ala Gly Gly Gly Tyr Trp His Thr Ser Gly Arg Glu Ile Leu Asp Ala
1               5                   10                  15
Asn Asn Val Pro Val Arg Ile Ala Gly Ile Asn Trp Phe Gly Phe Glu
                20                  25                  30
Thr Cys Asn Tyr Val Val His Gly Leu Trp Ser Arg Asp Tyr Arg Ser
                35                  40                  45
Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn Thr Ile Arg Leu Pro
        50                  55                  60
Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met Pro Asn Ser Ile Asn
65                  70                  75                  80
Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu Thr Ser Leu Gln Val
                85                  90                  95
Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile Gly Leu Arg Ile Ile
                100                 105                 110
Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln Ser Ala Leu Trp Tyr
        115                 120                 125
Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser Asp Leu Gln Ala Leu
        130                 135                 140
Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val Gly Phe Asp Leu His
145                 150                 155                 160
Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys Gly Asp Pro Ser Ile
```

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                   165                      170                      175
Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn Ala Val Leu Ser Val
            180                      185                      190
Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val Gln Ser Tyr Asn Gly
        195                      200                      205
Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly Ala Gly Gln Tyr Pro
    210                      215                      220
Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr Ser Ala His Asp Tyr
225                      230                      235                      240
Ala Thr Ser Val Tyr Pro Gln Thr Trp Phe Ser Asp Pro Thr Phe Pro
                245                      250                      255
Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp Gly Tyr Leu Phe Asn
            260                      265                      270
Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe Gly Thr Thr Leu Gln
        275                      280                      285
Ser Thr Thr Asp Gln Thr Trp Leu Lys Thr Leu Val Gln Tyr Leu Arg
        290                      295                      300
Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln Trp Thr Phe Trp Ser
305                      310                      315                      320
Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile Leu Lys Asp Asp Trp
                325                      330                      335
Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu Ala Pro Ile Lys Ser
            340                      345                      350
Ser Ile Phe Asp Pro Val Gly
            355


<210>  9
<211>  1914
<212>  DNA
<213>  Acidothermus cellulolyticus

<400>  9
aacgacccgt acatccagcg gttcctcacg atgtacaaca agattcacga cccagcgaac      60
ggctacttca gcccgcaggg aattccctac cactcggtag aaacgctcat cgttgaggca     120
ccggactacg ggcacgagac aacttcggag gcgtacagct tctggctctg gctcgaagcg     180
acgtacggcg cagtgaccgg caactggacg ccgttcaaca cgcctggac gacgatggaa     240
acgtacatga tcccgcagca cgcggaccag ccgaacaacg cgtcgtacaa ccccaacagc     300
ccggcgtcgt acgctccgga agagccgctg cccagcatgt acccggttgc catcgacagc     360
agcgtgccgg ttgggcacga cccgctcgcc gccgaattgc agtcgacgta cggcactccg     420
gacatttacg gcatgcactg gctggccgac gttgacaaca tctacggata cggcgacagc     480
cccggcggtg gttgcgaact cggtccttcc gctaagggcg tctcctacat caacacattc     540
cagcgcggct cgcaggagtc cgtctgggag acggtcaccc agccgacgtg cgacaacggc     600
aagtacggtg gggcgcacgg ctacgtcgac ctgttcatcc agggttcgac gccgccgcag     660
tggaagtaca ccgatgcccc ggacgccgac gcccgtgccg tccaggctgc gtactgggcc     720
tacacctggg catcggcgca gggcaaggca agcgcgattg ccccgacgat cgccaaggcg     780
gccaaactcg cgactacct gcggtactcg ctctttgaca agtacttcaa gcaggtcggc     840
aactgctacc cggccagctc ctgccctgga gcaaccggac gccagagcga gacctacctg     900
atcggctggt actacgcctg gggcggctca agccaaggct gggcctggcg cattggtgac     960
ggcgccgcgc acttcggcta ccagaatccg cttgccgcgt gggcgatgtc gaacgtgaca    1020
ccgctcattc cgctctcgcc cacggcaaag agcgactggg cggcgagctt gcagcgccag    1080
ctggagttct accagtggtt gcaatccgcg gaaggagcca ttgcgggcgg cgccaccaac    1140
agctggaacg gcaattacgg gaccccgccg gccggagact cgaccttcta cggcatggcg    1200
tacgactggg agccggtcta ccacgacccg ccgagcaaca actggttcgg cttccaggcg    1260
tggtccatgg aacgggttgc cgagtactac tacgtcaccg cgacccgaa ggccaaggcg    1320
ctgctcgaca agtgggtcgc atgggtgaag ccgaatgtca ccaccggtgc ctcatggtcg    1380
attccgtcga atttgtcctg gagcggccaa ccggatacct ggaatccgag caacccagga    1440
acgaatgcca acctgcacgt gaccatcacg tcgtccgggc aggacgtcgg tgttgccgcg    1500
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gcgctcgcga agacactcga gtactacgcg gcaaaatccg gcgatacggc ctcgcgcgac   1560
ctcgcgaagg gattgctcga ctccatgtgg aacaacgacc aggacagcct cggtgtgagc   1620
acaccggaga cgcggaccga ctactctcgg ttcactcagg tgtacgaccc gacgactggt   1680
gacggcctct acatcccgtc gggttggacg gggaccatgc ccaacggtga ccaaatcaag   1740
ccgggtgcga ccttcctgag catccggtcc tggtacacca aggatccgca gtggtcgaag   1800
gtgcaggcgt acctcaacgg cgggcctgct ccgacgttca actaccaccg gttctgggcg   1860
gagtccgact tcgcgatggc gaacgccgat tttggcatgc tcttcccatc cggg         1914
```

<210>    10
<211>    638
<212>    PRT
<213>    Acidothermus cellulolyticus

<400>    10

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Asn Asp Pro Tyr Ile Gln Arg Phe Leu Thr Met Tyr Asn Lys Ile His
 1               5                  10                  15
Asp Pro Ala Asn Gly Tyr Phe Ser Pro Gln Gly Ile Pro Tyr His Ser
                20                  25                  30
Val Glu Thr Leu Ile Val Glu Ala Pro Asp Tyr Gly His Glu Thr Thr
            35                  40                  45
Ser Glu Ala Tyr Ser Phe Trp Leu Trp Leu Glu Ala Thr Tyr Gly Ala
        50                  55                  60
Val Thr Gly Asn Trp Thr Pro Phe Asn Asn Ala Trp Thr Thr Met Glu
65                  70                  75                  80
Thr Tyr Met Ile Pro Gln His Ala Asp Gln Pro Asn Asn Ala Ser Tyr
                85                  90                  95
Asn Pro Asn Ser Pro Ala Ser Tyr Ala Pro Glu Glu Pro Leu Pro Ser
                100                 105                 110
Met Tyr Pro Val Ala Ile Asp Ser Ser Val Pro Val Gly His Asp Pro
        115                 120                 125
Leu Ala Ala Glu Leu Gln Ser Thr Tyr Gly Thr Pro Asp Ile Tyr Gly
    130                 135                 140
Met His Trp Leu Ala Asp Val Asp Asn Ile Tyr Gly Tyr Gly Asp Ser
145                 150                 155                 160
Pro Gly Gly Gly Cys Glu Leu Gly Pro Ser Ala Lys Gly Val Ser Tyr
                165                 170                 175
Ile Asn Thr Phe Gln Arg Gly Ser Gln Glu Ser Val Trp Glu Thr Val
             180                 185                 190
Thr Gln Pro Thr Cys Asp Asn Gly Lys Tyr Gly Gly Ala His Gly Tyr
        195                 200                 205
Val Asp Leu Phe Ile Gln Gly Ser Thr Pro Pro Gln Trp Lys Tyr Thr
    210                 215                 220
Asp Ala Pro Asp Ala Asp Ala Arg Ala Val Gln Ala Ala Tyr Trp Ala
225                 230                 235                 240
Tyr Thr Trp Ala Ser Ala Gln Gly Lys Ala Ser Ala Ile Ala Pro Thr
                245                 250                 255
Ile Ala Lys Ala Ala Lys Leu Gly Asp Tyr Leu Arg Tyr Ser Leu Phe
            260                 265                 270
Asp Lys Tyr Phe Lys Gln Val Gly Asn Cys Tyr Pro Ala Ser Ser Cys
        275                 280                 285
Pro Gly Ala Thr Gly Arg Gln Ser Glu Thr Tyr Leu Ile Gly Trp Tyr
        290                 295                 300
Tyr Ala Trp Gly Gly Ser Ser Gln Gly Trp Ala Trp Arg Ile Gly Asp
305                 310                 315                 320
Gly Ala Ala His Phe Gly Tyr Gln Asn Pro Leu Ala Ala Trp Ala Met
                325                 330                 335
Ser Asn Val Thr Pro Leu Ile Pro Leu Ser Pro Thr Ala Lys Ser Asp
```

```
                      340                        345                        350
Trp Ala Ala Ser Leu Gln Arg Gln Leu Glu Phe Tyr Gln Trp Leu Gln
              355                        360                   365
Ser Ala Glu Gly Ala Ile Ala Gly Gly Ala Thr Asn Ser Trp Asn Gly
          370                        375                   380
Asn Tyr Gly Thr Pro Pro Ala Gly Asp Ser Thr Phe Tyr Gly Met Ala
385                        390                        395                   400
Tyr Asp Trp Glu Pro Val Tyr His Asp Pro Pro Ser Asn Asn Trp Phe
                  405                        410                        415
Gly Phe Gln Ala Trp Ser Met Glu Arg Val Ala Glu Tyr Tyr Tyr Val
              420                        425                   430
Thr Gly Asp Pro Lys Ala Lys Ala Leu Leu Asp Lys Trp Val Ala Trp
          435                        440                   445
Val Lys Pro Asn Val Thr Thr Gly Ala Ser Trp Ser Ile Pro Ser Asn
          450                        455                   460
Leu Ser Trp Ser Gly Gln Pro Asp Thr Trp Asn Pro Ser Asn Pro Gly
465                        470                        475                   480
Thr Asn Ala Asn Leu His Val Thr Ile Thr Ser Ser Gly Gln Asp Val
                  485                        490                        495
Gly Val Ala Ala Ala Leu Ala Lys Thr Leu Glu Tyr Tyr Ala Ala Lys
              500                        505                   510
Ser Gly Asp Thr Ala Ser Arg Asp Leu Ala Lys Gly Leu Leu Asp Ser
          515                        520                   525
Met Trp Asn Asn Asp Gln Asp Ser Leu Gly Val Ser Thr Pro Glu Thr
          530                        535                   540
Arg Thr Asp Tyr Ser Arg Phe Thr Gln Val Tyr Asp Pro Thr Thr Gly
545                        550                        555                   560
Asp Gly Leu Tyr Ile Pro Ser Gly Trp Thr Gly Thr Met Pro Asn Gly
                  565                        570                   575
Asp Gln Ile Lys Pro Gly Ala Thr Phe Leu Ser Ile Arg Ser Trp Tyr
              580                        585                   590
Thr Lys Asp Pro Gln Trp Ser Lys Val Gln Ala Tyr Leu Asn Gly Gly
          595                        600                   605
Pro Ala Pro Thr Phe Asn Tyr His Arg Phe Trp Ala Glu Ser Asp Phe
      610                        615                   620
Ala Met Ala Asn Ala Asp Phe Gly Met Leu Phe Pro Ser Gly
625                        630                   635

<210>   11
<211>   2223
<212>   DNA
<213>   Acidothermus cellulolyticus

<400>   11
gcgacgactc agccgtacac ctggagcaac gtggcgatcg ggggcggcgg ctttgtcgac   60
gggatcgtct tcaatgaagg tgcaccggga attctgtacg tgcggacgga catcggggggg   120
atgtatcgat gggatgccgc caacgggcgg tggatccctc ttctggattg ggtgggatgg   180
aacaattggg ggtacaacgg cgtcgtcagc attgcggcag acccgatcaa tactaacaag   240
gtatgggccg ccgtcggaat gtacaccaac agctgggacc caaacgacgg agcgattctc   300
cgctcgtctg atcagggcgc aacgtggcaa ataacgcccc tgccgttcaa gcttggcggc   360
aacatgcccg ggcgtggaat gggcgagcgg cttgcggtgg atccaaacaa tgacaacatt   420
ctgtatttcg cgccccgag cggcaaaggg ctctggagaa gcacagattc cggcgcgacc   480
tggtcccaga tgacgaactt tccggacgta ggcacgtaca ttgcaaatcc cactgacacg   540
accggctatc agagcgatat tcaaggcgtc gtctgggtcg ctttcgacaa gtcttcgtca   600
tcgctcgggc aagcgagtaa gaccattttt gtgggcgtgg cggatcccaa taatccggtc   660
ttctggagca gagacggcgg cgcgacgtgg caggcggtgc cgggtgcgcc gaccggcttc   720
atcccgcaca agggcgtctt tgacccggtc aaccacgtgc tctatattgc caccagcaat   780
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acgggtggtc cgtatgacgg gagctccggc gacgtctgga aattctcggt gacctccggg    840
acatggacgc gaatcagccc ggtaccttcg acggacacgg ccaacgacta ctttggttac    900
agcggcctca ctatcgaccg ccagcacccg aacacgataa tggtggcaac ccagatatcg    960
tggtggccgg acaccataat ctttcggagc accgacggcg gtgcgacgtg gacgcggatc   1020
tgggattgga cgagttatcc caatcgaagc ttgcgatatg tgcttgacat ttcggcggag   1080
ccttggctga ccttcggcgt cagccgaat  cctcccgtac cgagtccgaa gctcggctgg   1140
atggatgaag cgatggcaat cgatccgttc aactctgatc ggatgctcta cggaacaggc   1200
gcgacgttgt acgcaacaaa tgatctcacg aagtgggact ccggcggcca gattcatatc   1260
gcgccgatgg tcaaaggatt ggaggagacg gcggtaaacg atctcatcag cccgccgtct   1320
ggcgccccgc tcatcagcgc tctcggagac ctcggcggct cacccacgc  cgacgttact   1380
gccgtgccat cgacgatctt cacgtcaccg gtgttcacga ccggcaccag cgtcgactat   1440
gcggaattga atccgtcgat catcgttcgc gctggaagtt tcgatccatc gagccaaccg   1500
aacgacaggc acgtcgcgtt ctcgacagac ggcggcaaga actggttcca aggcagcgaa   1560
cctggcgggg tgacgacggg cggcaccgtc gccgcatcgg ccgacggctc tcgtttcgtc   1620
tgggctcccg gcgatccgg  tcagcctgtg gtgtacgcag tcggatttgg caactcctgg   1680
gctgcttcgc aaggtgttcc cgccaatgcc cagatccgct cagaccgggt gaatccaaag   1740
actttctatg ccctatccaa tggaaccttc tatcgaagca cggacggcgg cgtgacattc   1800
caaccggtcg cggccggtct tccgagcagc ggtgccgtcg gtgtcatgtt ccacgcggtg   1860
cctggaaaag aaggcgatct gtggctcgct gcatcgagcg ggctttacca ctcaaccaat   1920
ggcggcagca gttggtctgc aatcaccggc gtatcctccg cggtgaacgt gggatttggt   1980
aagtctgcgc ccgggtcgtc atacccagcc gtctttgtcg tcggcacgat cggaggcgtt   2040
acgggggcgt accgctccga cgacggtggg acgacctggg tacggatcaa tgatgaccag   2100
caccaatacg gaaattgggg acaagcaatc accggtgacc cgcgaattta cgggcgggtg   2160
tacataggca cgaacggccg tggaattgtc tacggggaca ttggtggtgc gccgtccgga   2220
·tcg                                                                2223

<210>   12
<211>   741
<212>   PRT
<213>   Acidothermus cellulolyticus

<400>   12
Ala Thr Thr Gln Pro Tyr Thr Trp Ser Asn Val Ala Ile Gly Gly Gly
1               5                   10                  15
Gly Phe Val Asp Gly Ile Val Phe Asn Glu Gly Ala Pro Gly Ile Leu
            20                  25                  30
Tyr Val Arg Thr Asp Ile Gly Gly Met Tyr Arg Trp Asp Ala Ala Asn
        35                  40                  45
Gly Arg Trp Ile Pro Leu Leu Asp Trp Val Gly Trp Asn Asn Trp Gly
    50                  55                  60
Tyr Asn Gly Val Val Ser Ile Ala Ala Asp Pro Ile Asn Thr Asn Lys
65                  70                  75                  80
Val Trp Ala Ala Val Gly Met Tyr Thr Asn Ser Trp Asp Pro Asn Asp
                85                  90                  95
Gly Ala Ile Leu Arg Ser Ser Asp Gln Gly Ala Thr Trp Gln Ile Thr
            100                 105                 110
Pro Leu Pro Phe Lys Leu Gly Gly Asn Met Pro Gly Arg Gly Met Gly
        115                 120                 125
Glu Arg Leu Ala Val Asp Pro Asn Asn Asp Asn Ile Leu Tyr Phe Gly
        130                 135                 140
Ala Pro Ser Gly Lys Gly Leu Trp Arg Ser Thr Asp Ser Gly Ala Thr
145                 150                 155                 160
Trp Ser Gln Met Thr Asn Phe Pro Asp Val Gly Thr Tyr Ile Ala Asn
                165                 170                 175
Pro Thr Asp Thr Thr Gly Tyr Gln Ser Asp Ile Gln Gly Val Val Trp
            180                 185                 190
Val Ala Phe Asp Lys Ser Ser Ser Ser Leu Gly Gln Ala Ser Lys Thr
```

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              195                     200                     205
Ile Phe Val Gly Val Ala Asp Pro Asn Asn Pro Val Phe Trp Ser Arg
    210                     215                     220
Asp Gly Gly Ala Thr Trp Gln Ala Val Pro Gly Ala Pro Thr Gly Phe
225                     230                     235                     240
Ile Pro His Lys Gly Val Phe Asp Pro Val Asn His Val Leu Tyr Ile
                245                     250                     255
Ala Thr Ser Asn Thr Gly Gly Pro Tyr Asp Gly Ser Ser Gly Asp Val
                260                     265                     270
Trp Lys Phe Ser Val Thr Ser Gly Thr Trp Thr Arg Ile Ser Pro Val
                275                     280                     285
Pro Ser Thr Asp Thr Ala Asn Asp Tyr Phe Gly Tyr Ser Gly Leu Thr
                290                     295                     300
Ile Asp Arg Gln His Pro Asn Thr Ile Met Val Ala Thr Gln Ile Ser
305                     310                     315                     320
Trp Trp Pro Asp Thr Ile Ile Phe Arg Ser Thr Asp Gly Gly Ala Thr
                325                     330                     335
Trp Thr Arg Ile Trp Asp Trp Thr Ser Tyr Pro Asn Arg Ser Leu Arg
                340                     345                     350
Tyr Val Leu Asp Ile Ser Ala Glu Pro Trp Leu Thr Phe Gly Val Gln
                355                     360                     365
Pro Asn Pro Pro Val Pro Ser Pro Lys Leu Gly Trp Met Asp Glu Ala
    370                     375                     380
Met Ala Ile Asp Pro Phe Asn Ser Asp Arg Met Leu Tyr Gly Thr Gly
385                     390                     395                     400
Ala Thr Leu Tyr Ala Thr Asn Asp Leu Thr Lys Trp Asp Ser Gly Gly
                405                     410                     415
Gln Ile His Ile Ala Pro Met Val Lys Gly Leu Glu Glu Thr Ala Val
                420                     425                     430
Asn Asp Leu Ile Ser Pro Pro Ser Gly Ala Pro Leu Ile Ser Ala Leu
                435                     440                     445
Gly Asp Leu Gly Gly Phe Thr His Ala Asp Val Thr Ala Val Pro Ser
    450                     455                     460
Thr Ile Phe Thr Ser Pro Val Phe Thr Thr Gly Thr Ser Val Asp Tyr
465                     470                     475                     480
Ala Glu Leu Asn Pro Ser Ile Ile Val Arg Ala Gly Ser Phe Asp Pro
                485                     490                     495
Ser Ser Gln Pro Asn Asp Arg His Val Ala Phe Ser Thr Asp Gly Gly
                500                     505                     510
Lys Asn Trp Phe Gln Gly Ser Glu Pro Gly Gly Val Thr Thr Gly Gly
                515                     520                     525
Thr Val Ala Ala Ser Ala Asp Gly Ser Arg Phe Val Trp Ala Pro Gly
    530                     535                     540
Asp Pro Gly Gln Pro Val Val Tyr Ala Val Gly Phe Gly Asn Ser Trp
545                     550                     555                     560
Ala Ala Ser Gln Gly Val Pro Ala Asn Ala Gln Ile Arg Ser Asp Arg
                565                     570                     575
Val Asn Pro Lys Thr Phe Tyr Ala Leu Ser Asn Gly Thr Phe Tyr Arg
                580                     585                     590
Ser Thr Asp Gly Gly Val Thr Phe Gln Pro Val Ala Ala Gly Leu Pro
                595                     600                     605
Ser Ser Gly Ala Val Gly Val Met Phe His Ala Val Pro Gly Lys Glu
    610                     615                     620
Gly Asp Leu Trp Leu Ala Ala Ser Ser Gly Leu Tyr His Ser Thr Asn
625                     630                     635                     640
Gly Gly Ser Ser Trp Ser Ala Ile Thr Gly Val Ser Ser Ala Val Asn
                645                     650                     655
```

Val Gly Phe Gly Lys Ser Ala Pro Gly Ser Ser Tyr Pro Ala Val Phe
            660                 665                 670
Val Val Gly Thr Ile Gly Gly Val Thr Gly Ala Tyr Arg Ser Asp Asp
        675                 680                 685
Gly Gly Thr Thr Trp Val Arg Ile Asn Asp Asp Gln His Gln Tyr Gly
    690                 695                 700
Asn Trp Gly Gln Ala Ile Thr Gly Asp Pro Arg Ile Tyr Gly Arg Val
705                 710                 715                 720
Tyr Ile Gly Thr Asn Gly Arg Gly Ile Val Tyr Gly Asp Ile Gly Gly
                725                 730                 735
Ala Pro Ser Gly Ser
            740

<210>   13
<211>   1677
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   construct based on Thermobifida fusca

<400>   13
gccggctgct cggtggacta cacggtcaac tcctggggta ccgggttcac cgccaacgtc      60
accatcacca acctcggcag tgcgatcaac ggctggaccc tggagtggga cttccccggc     120
aaccagcagg tgaccaacct gtggaacggg acctacaccc agtccgggca gcacgtgtcg     180
gtcagcaacg ccccgtacaa cgcctccatc ccggccaacg gaacggttga gttcgggttc     240
aacggctcct actcgggcag caacgacatc ccctcctcct tcaagctgaa cggggttacc     300
tgcgacggct cggacgaccc cgaccccgag cccagcccct ccccagccc ttcccccagc      360
cccacagacc cggatgagcc gggcggcccg accaacccgc ccaccaaccc cggcgagaag     420
gtcgacaacc cgttcgaggg cgccaagctg tacgtgaacc cggtctggtc ggccaaggcc     480
gccgctgagc cgggcggttc cgcggtcgcc aacgagtcca ccgctgtctg gctggaccgt     540
atcggcgcca tcgagggcaa cgacagcccg accaccggct ccatgggtct cgcgcgaccac     600
ctggaggagg ccgtccgcca gtccggtggc gacccgctga ccatccaggt cgtcatctac     660
aacctgcccg gccgcgactg cgccgcgctg gcctccaacg gtgagctggg tcccgatgaa     720
ctcgaccgct acaagagcga gtacatcgac ccgatcgccg acatcatgtg ggacttcgca     780
gactacgaga acctgcggat cgtcgccatc atcgagatcg actccctgcc caacctcgtc     840
accaacgtgg cgggaacggg cggcaccgag ctctgcgcct acatgaagca gaacggcggc     900
tacgtcaacg tgtcggcta cgccctccgc aagctgggcg agatcccgaa cgtctacaac      960
tacatcgacg ccgcccacca cggctggatc ggctgggact ccaacttcgg ccccctcggtg   1020
gacatcttct acgaggccgc caacgcctcc ggctccaccg tggactacgt gcacggcttc    1080
atctccaaca cggccaacta ctcggccact gtggagccgt acctggacgt caacggcacc    1140
gttaacggcc agctcatccg ccagtccaag tgggttgact ggaaccagta cgtcgacgag    1200
ctctccttcg tccaggacct gcgtcaggcc ctgatcgcca agggcttccg gtccgacatc    1260
ggtatgctca tcgacacctc ccgcaacggc tggggtggcc cgaaccgtcc gaccggaccg    1320
agctcctcca ccgacctcaa cacctacgtt gacgagagcc gtatcgaccg ccgtatccac    1380
cccggtaact ggtgcaacca ggccggtgcg ggcctcggcg agcggcccac ggtcaacccg    1440
gctcccggtg ttgacgccta cgtctgggtg aagccccgg gtgagtccga cggcgccagc     1500
gaggagatcc cgaacgacga gggcaagggc ttcgaccgca tgtgcgaccc gacctaccag    1560
ggcaacgccc gcaacggcaa caacccctcg ggtgcgctgc caacgccccc catctccggc    1620
cactggttct ctgcccagtt ccgcgagctg ctggccaacg cctacccgcc tctgtaa       1677

<210>   14
<211>   558
<212>   PRT
<213>   Artificial Sequence

<220>

<223> construct based on Thermobifida fusca

<400> 14
Ala Gly Cys Ser Val Asp Tyr Thr Val Asn Ser Trp Gly Thr Gly Phe
1               5                   10                  15
Thr Ala Asn Val Thr Ile Thr Asn Leu Gly Ser Ala Ile Asn Gly Trp
            20                  25                  30
Thr Leu Glu Trp Asp Phe Pro Gly Asn Gln Gln Val Thr Asn Leu Trp
        35                  40                  45
Asn Gly Thr Tyr Thr Gln Ser Gly Gln His Val Ser Val Ser Asn Ala
    50                  55                  60
Pro Tyr Asn Ala Ser Ile Pro Ala Asn Gly Thr Val Glu Phe Gly Phe
65                  70                  75                  80
Asn Gly Ser Tyr Ser Gly Ser Asn Asp Ile Pro Ser Ser Phe Lys Leu
                85                  90                  95
Asn Gly Val Thr Cys Asp Gly Ser Asp Asp Pro Asp Pro Glu Pro Ser
            100                 105                 110
Pro Ser Pro Ser Pro Ser Pro Ser Pro Thr Asp Pro Asp Glu Pro Gly
        115                 120                 125
Gly Pro Thr Asn Pro Pro Thr Asn Pro Gly Glu Lys Val Asp Asn Pro
    130                 135                 140
Phe Glu Gly Ala Lys Leu Tyr Val Asn Pro Val Trp Ser Ala Lys Ala
145                 150                 155                 160
Ala Ala Glu Pro Gly Gly Ser Ala Val Ala Asn Glu Ser Thr Ala Val
            165                 170             175
Trp Leu Asp Arg Ile Gly Ala Ile Glu Gly Asn Asp Ser Pro Thr Thr
            180                 185                 190
Gly Ser Met Gly Leu Arg Asp His Leu Glu Glu Ala Val Arg Gln Ser
        195                 200                 205
Gly Gly Asp Pro Leu Thr Ile Gln Val Val Ile Tyr Asn Leu Pro Gly
    210                 215                 220
Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Gly Pro Asp Glu
225                 230                 235                 240
Leu Asp Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala Asp Ile Met
            245                 250                 255
Trp Asp Phe Ala Asp Tyr Glu Asn Leu Arg Ile Val Ala Ile Ile Glu
            260                 265                 270
Ile Asp Ser Leu Pro Asn Leu Val Thr Asn Val Gly Gly Asn Gly Gly
        275                 280                 285
Thr Glu Leu Cys Ala Tyr Met Lys Gln Asn Gly Gly Tyr Val Asn Gly
    290                 295                 300
Val Gly Tyr Ala Leu Arg Lys Leu Gly Glu Ile Pro Asn Val Tyr Asn
305                 310                 315                 320
Tyr Ile Asp Ala Ala His His Gly Trp Ile Gly Trp Asp Ser Asn Phe
            325                 330                 335
Gly Pro Ser Val Asp Ile Phe Tyr Glu Ala Ala Asn Ala Ser Gly Ser
            340                 345                 350
Thr Val Asp Tyr Val His Gly Phe Ile Ser Asn Thr Ala Asn Tyr Ser
        355                 360                 365
Ala Thr Val Glu Pro Tyr Leu Asp Val Asn Gly Thr Val Asn Gly Gln
    370                 375                 380
Leu Ile Arg Gln Ser Lys Trp Val Asp Trp Asn Gln Tyr Val Asp Glu
385                 390                 395                 400
Leu Ser Phe Val Gln Asp Leu Arg Gln Ala Leu Ile Ala Lys Gly Phe
                405                 410                 415
Arg Ser Asp Ile Gly Met Leu Ile Asp Thr Ser Arg Asn Gly Trp Gly
            420                 425                 430

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Gly Pro Asn Arg Pro Thr Gly Pro Ser Ser Ser Thr Asp Leu Asn Thr
        435                 440                 445
Tyr Val Asp Glu Ser Arg Ile Asp Arg Arg Ile His Pro Gly Asn Trp
        450                 455                 460
Cys Asn Gln Ala Gly Ala Gly Leu Gly Glu Arg Pro Thr Val Asn Pro
465                 470                 475                 480
Ala Pro Gly Val Asp Ala Tyr Val Trp Val Lys Pro Pro Gly Glu Ser
                485                 490                 495
Asp Gly Ala Ser Glu Glu Ile Pro Asn Asp Glu Gly Lys Gly Phe Asp
                500                 505                 510
Arg Met Cys Asp Pro Thr Tyr Gln Gly Asn Ala Arg Asn Gly Asn Asn
        515                 520                 525
Pro Ser Gly Ala Leu Pro Asn Ala Pro Ile Ser Gly His Trp Phe Ser
        530                 535                 540
Ala Gln Phe Arg Glu Leu Leu Ala Asn Ala Tyr Pro Pro Leu
545                 550                 555

<210>   15
<211>   1293
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   construct based on Thermobifida fusca

<400>   15
gccggtctca ccgccacagt caccaaagaa tcctcgtggg acaacggcta ctccgcgtcc      60
gtcaccgtcc gcaacgacac ctcgagcacc gtctcccagt gggaggtcgt cctcaccctg     120
cccggcggca ctacagtggc ccaggtgtgg aacgcccagc acaccagcag cggcaactcc     180
cacaccttca ccggggtttc ctggaacagc accatcccgc ccggaggcac cgcctcttcc     240
ggcttcatcg cttccggcag cggcgaaccc acccactgca ccatcaacgg cgcccccctgc    300
gacgaaggct ccgagccggg cggcccccggc ggtcccggaa cccccctcccc cgaccccggc    360
acgcagcccg gcaccggcac cccggtcgag cggtacggca aagtccaggt ctgcggcacc     420
cagctctgcg acgagcacgg caacccggtc caactgcgcg gcatgagcac ccacggcatc     480
cagtggttcg accactgcct gaccgacagc tcgctggacg ccctggccta cgactggaag     540
gccgacatca tccgcctgtc catgtacatc caggaagacg gctacgagac caacccgcgc     600
ggcttcaccg accggatgca ccagctcatc gacatggcca cggcgcgcgg cctgtacgtg     660
atcgtggact ggcacatcct caccccgggc gatccccact acaacctgga ccgggccaag     720
accttcttcg cggaaatcgc ccagcgccac gccagcaaga ccaacgtgct ctacgagatc     780
gccaacgaac caacggagt gagctgggcc tccatcaaga gctacgccga gaggtcatc      840
ccggtgatcc gccagcgcga ccccgactcg gtgatcatcg tgggcacccg cggctggtcg     900
tcgctcggcg tctccgaagg ctccggcccc gccgagatcg cggccaaccc ggtcaacgcc     960
tccaacatca tgtacgcctt ccacttctac gcggcctcgc accgcgacaa ctacctcaac    1020
gcgctgcgtg aggcctccga gctgttcccg gtcttcgtca ccgagttcgg caccgagacc    1080
tacaccggtg acggcgccaa cgacttccag atggccgacc gctacatcga cctgatggcg    1140
gaacggaaga tcgggtggac caagtggaac tactcggacg acttccgttc cggcgcggtc    1200
ttccagccgg gcacctgcgc gtccggcggc ccgtggagcg gttcgtcgct gaaggcgtcc    1260
ggacagtggg tgcggagcaa gctccagtcc tga                                 1293

<210>   16
<211>   430
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   construct based on Thermobifida fusca
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<400> 16
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Ala Gly Leu Thr Ala Thr Val Thr Lys Glu Ser Ser Trp Asp Asn Gly
1               5                   10                  15
Tyr Ser Ala Ser Val Thr Val Arg Asn Asp Thr Ser Ser Thr Val Ser
            20                  25                  30
Gln Trp Glu Val Val Leu Thr Leu Pro Gly Gly Thr Thr Val Ala Gln
        35                  40                  45
Val Trp Asn Ala Gln His Thr Ser Ser Gly Asn Ser His Thr Phe Thr
    50                  55                  60
Gly Val Ser Trp Asn Ser Thr Ile Pro Pro Gly Gly Thr Ala Ser Ser
65                  70                  75                  80
Gly Phe Ile Ala Ser Gly Ser Gly Glu Pro Thr His Cys Thr Ile Asn
                85                  90                  95
Gly Ala Pro Cys Asp Glu Gly Ser Glu Pro Gly Gly Pro Gly Gly Pro
            100                 105                 110
Gly Thr Pro Ser Pro Asp Pro Gly Thr Gln Pro Gly Thr Gly Thr Pro
        115                 120                 125
Val Glu Arg Tyr Gly Lys Val Gln Val Cys Gly Thr Gln Leu Cys Asp
    130                 135                 140
Glu His Gly Asn Pro Val Gln Leu Arg Gly Met Ser Thr His Gly Ile
145                 150                 155                 160
Gln Trp Phe Asp His Cys Leu Thr Asp Ser Ser Leu Asp Ala Leu Ala
            165                 170                 175
Tyr Asp Trp Lys Ala Asp Ile Ile Arg Leu Ser Met Tyr Ile Gln Glu
            180                 185                 190
Asp Gly Tyr Glu Thr Asn Pro Arg Gly Phe Thr Asp Arg Met His Gln
        195                 200                 205
Leu Ile Asp Met Ala Thr Ala Arg Gly Leu Tyr Val Ile Val Asp Trp
    210                 215                 220
His Ile Leu Thr Pro Gly Asp Pro His Tyr Asn Leu Asp Arg Ala Lys
225                 230                 235                 240
Thr Phe Phe Ala Glu Ile Ala Gln Arg His Ala Ser Lys Thr Asn Val
            245                 250                 255
Leu Tyr Glu Ile Ala Asn Glu Pro Asn Gly Val Ser Trp Ala Ser Ile
            260                 265                 270
Lys Ser Tyr Ala Glu Glu Val Ile Pro Val Ile Arg Gln Arg Asp Pro
        275                 280                 285
Asp Ser Val Ile Ile Val Gly Thr Arg Gly Trp Ser Ser Leu Gly Val
        290                 295                 300
Ser Glu Gly Ser Gly Pro Ala Glu Ile Ala Ala Asn Pro Val Asn Ala
305                 310                 315                 320
Ser Asn Ile Met Tyr Ala Phe His Phe Tyr Ala Ala Ser His Arg Asp
            325                 330                 335
Asn Tyr Leu Asn Ala Leu Arg Glu Ala Ser Glu Leu Phe Pro Val Phe
        340                 345                 350
Val Thr Glu Phe Gly Thr Glu Thr Tyr Thr Gly Asp Gly Ala Asn Asp
    355                 360                 365
Phe Gln Met Ala Asp Arg Tyr Ile Asp Leu Met Ala Glu Arg Lys Ile
    370                 375                 380
Gly Trp Thr Lys Trp Asn Tyr Ser Asp Asp Phe Arg Ser Gly Ala Val
385                 390                 395                 400
Phe Gln Pro Gly Thr Cys Ala Ser Gly Gly Pro Trp Ser Gly Ser Ser
            405                 410                 415
Leu Lys Ala Ser Gly Gln Trp Val Arg Ser Lys Leu Gln Ser
            420                 425                 430
```

<210> 17

<211> 2656
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion construct

<400> 17
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atgtatcgga agttggccgt catctcggcc ttcttggcca cagctcgtgc tcagtcggcc      60
tgcactctcc aatcggagac tcacccgcct ctgacatggc agaaatgctc gtctggtggc     120
acttgcactc aacagacagg ctccgtggtc atcgacgcca actggcgctg gactcacgct     180
acgaacagca gcacgaactg ctacgatggc aacacttgga gctcgaccct atgtcctgac     240
aacgagacct gcgcgaagaa ctgctgtctg gacggtgccg cctacgcgtc cacgtacgga     300
gttaccacga gcggtaacag cctctccatt ggctttgtca cccagtctgc cagaagaac      360
gttggcgctc gcctttacct tatggcgagc gacacgacct accaggaatt caccctgctt     420
ggcaacgagt tctctttcga tgttgatgtt tcgcagctgc cgtaagtgac ttaccatgaa     480
cccctgacgt atcttcttgt gggctcccag ctgactggcc aatttaaggt gcggcttgaa     540
cggagctctc tacttcgtgt ccatggacgc ggatggtggc gtgagcaagt atcccaccaa     600
caccgctggc gccaagtacg gcacggggta ctgtgacagc cagtgtcccc gcgatctgaa     660
gttcatcaat ggccaggcca acgttgaggg ctgggagccg tcatccaaca acgcaaacac     720
gggcattgga ggacacggaa gctgctgctc tgagatggat atctgggagg ccaactccat     780
ctccgaggct cttacccccc acccttgcac gactgtcggc caggagatct gcgagggtga     840
tgggtgcggc ggaacttact ccgataacag atatggcggc acttgcgatc ccgatggctg     900
cgactggaac ccataccgcc tgggcaacac cagcttctac ggccctggct caagctttac     960
cctcgatacc accaagaaat tgaccgttgt cacccagttc gagacgtcgg gtgccatcaa    1020
ccgatactat gtccagaatg cgtcactttt ccagcagccc aacgccgagc ttggtagtta    1080
ctctggcaac gagctcaacg atgattactg cacagctgag gaggcagaat cggcggatc     1140
ctctttctca gacaagggcg gcctgactca gttcaagaag ctacctctg gcggcatggt    1200
tctggtcatg agtctgtggg atgatgtgag tttgatggac aaacatgcgc gttgacaaag    1260
agtcaagcag ctgactgaga tgttacagta ctacgccaac atgctgtggc tggactccac    1320
ctacccgaca aacgagacct cctccacacc cggtgccgtg cgcggaagct gctccaccag    1380
ctccggtgtc cctgctcagg tcgaatctca gtctcccaac gccaaggtca ccttctccaa    1440
catcaagttc ggacccattg gcagcaccgg caaccctagc ggcggcaacc ctcccggcgg    1500
aaacccgcct ggcaccacca ccacccgccg cccagccact accactggaa gctctcccgg    1560
acctactagt aagcgggcgg cggcggcta ttggcacacg agcggccggg agatcctgga    1620
cgcgaacaac gtgccggtac ggatcgccgg catcaactgg tttgggttcg aaacctgcaa    1680
ttacgtcgtg cacggtctct ggtcacgcga ctaccgcagc atgctcgacc agataaagtc    1740
gctcggctac aacacaatcc ggctgccgta ctctgacgac attctcaagc cgggcaccat    1800
gccgaacagc atcaattttt accagatgaa tcaggacctg cagggtctga cgtccttgca    1860
ggtcatggac aaaatcgtcg cgtacgccgg tcagatcggc ctgcgcatca ttcttgaccg    1920
ccaccgaccg gattgcagcg ggcagtcggc gctgtggtac acgagcagcg tctcggaggc    1980
tacgtggatt tccgacctgc aagcgctggc gcagcgctac aagggaaacc cgacggtcgt    2040
cggctttgac ttgcacaacg agccgcatga cccggcctgc tggggctgcg cgatccgag     2100
catcgactgg cgattggccg ccgagcgggc cggaaacgcc gtgctctcgg tgaatccgaa    2160
cctgctcatt ttcgtcgaag gtgtgcagag ctacaacgga gactcctact ggtggggcgg    2220
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Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
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Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
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Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
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\<400\>  20
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21